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#1



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/517,491

DATE: 02/28/2002

TIME: 14:57:34

Input Set : N:\Crf3\RULE60\09517491.raw
 Output Set: N:\CRF3\02282002\I517491.raw

SEQUENCE LISTING

- 3 (1) GENERAL INFORMATION:
 - 5 (i) APPLICANT: Berlin, Vivian
Chiu, Maria Isabel
Cottarel, Guillaume
Damagnez, Veronique
 - 10 (ii) TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
 - 12 (iii) NUMBER OF SEQUENCES: 35
 - 14 (iv) CORRESPONDENCE ADDRESS:
 - 15 (A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 - 16 (B) STREET: One Post Office Square
 - 17 (C) CITY: Boston
 - 18 (D) STATE: MA
 - 19 (E) COUNTRY: USA
 - 20 (F) ZIP: 02109-2170
 - 22 (v) COMPUTER READABLE FORM:
 - 23 (A) MEDIUM TYPE: Floppy disk
 - 24 (B) COMPUTER: IBM PC compatible
 - 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - 28 (vi) CURRENT APPLICATION DATA:
 - 29 (A) APPLICATION NUMBER: US/09/517,491
 - 30 (B) FILING DATE: 02-Mar-2000
 - 31 (C) CLASSIFICATION:
 - 33 (vii) PRIOR APPLICATION DATA:
 - 34 (A) APPLICATION NUMBER: 08/360,144
 - 35 (B) FILING DATE: 20-DEC-1994
 - 39 (viii) ATTORNEY/AGENT INFORMATION:
 - 40 (A) NAME: Vincent, Matthew P.
 - 41 (B) REGISTRATION NUMBER: 36,709
 - 42 (C) REFERENCE/DOCKET NUMBER: APV-036.02
 - 44 (ix) TELECOMMUNICATION INFORMATION:
 - 45 (A) TELEPHONE: 617-832-1000
 - 46 (B) TELEFAX: 617-832-7000
 - 49 (2) INFORMATION FOR SEQ ID NO: 1:
 - 51 (i) SEQUENCE CHARACTERISTICS:
 - 52 (A) LENGTH: 486 base pairs
 - 53 (B) TYPE: nucleic acid
 - 54 (C) STRANDEDNESS: both
 - 55 (D) TOPOLOGY: linear
 - 57 (ii) MOLECULE TYPE: cDNA
 - 60 (ix) FEATURE:
 - 61 (A) NAME/KEY: CDS

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62 (B) LOCATION: 1..486
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 67 CTC ACC CGT CAC AAT GCA GCC AAC AAG ATC TTG AAG AAC ATG TGT GAA 48
 68 Leu Thr Arg His Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu
 69 1 5 10 15
 71 CAC AGC AAC ACG CTG GTC CAG CAG GCC ATG ATG GTG AGT GAA GAG CTG 96
 72 His Ser Asn Thr Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu
 73 20 25 30
 75 ATT CGG GTA GCC ATC CTC TGG CAT GAG ATG TGG CAT GAA GGC CTG GAA 144
 76 Ile Arg Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu
 77 35 40 45
 79 GAG GCA TCT CGC TTG TAC TTT GGG GAG AGG AAC GTG AAA GGC ATG TTT 192
 80 Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe
 81 50 55 60
 83 GAG GTG CTG GAG CCC CTG CAT GCT ATG ATG GAA CGG GGT CCC CGG ACT 240
 84 Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Arg Thr
 85 65 70 75 80
 87 CTG AAG GAA ACA TCC TTT AAT CAG GCA TAT GGC CGA GAT TTA ATG GAG 288
 88 Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu
 89 85 90 95
 91 GCA CAA GAA TGG TGT CGA AAG TAC ATG AAG TCG GGG AAC GTC AAG GAC 336
 92 Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp
 93 100 105 110
 95 CTC ACG CAA GCC TGG GAC CTC TAC TAT CAC GTG TTC AGA CGG ATC TCA 384
 96 Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
 97 115 120 125
 99 AAG CAG CTA CCC CAG CTC ACA TCC CTG GAG CTG CAG TAT GTG TCC CCC 432
 100 Lys Gln Leu Pro Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro
 101 130 135 140
 103 AAA CTT CTG ATG TGC CGA GAC CTT GAG TTG GCT GTG CCA GGA ACA TAC 480
 104 Lys Leu Leu Met Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr
 105 145 150 155 160
 107 GAC CCC 486
 108 Asp Pro
 112 (2) INFORMATION FOR SEQ ID NO: 2:
 114 (i) SEQUENCE CHARACTERISTICS:
 115 (A) LENGTH: 162 amino acids
 116 (B) TYPE: amino acid
 117 (D) TOPOLOGY: linear
 119 (ii) MOLECULE TYPE: protein
 121 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 123 Leu Thr Arg His Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu
 124 1 5 10 15
 126 His Ser Asn Thr Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu
 127 20 25 30
 129 Ile Arg Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu
 130 35 40 45
 132 Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe
 133 50 55 60

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135 Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Arg Thr
136 65 70 75 80
138 Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu
139 85 90 95
141 Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp
142 100 105 110
144 Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
145 115 120 125
147 Lys Gln Leu Pro Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro
148 130 135 140
150 Lys Leu Leu Met Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr
151 145 150 155 160
153 Asp Pro

156 (2) INFORMATION FOR SEQ ID NO: 3:
158 (i) SEQUENCE CHARACTERISTICS:

159 (A) LENGTH: 40 base pairs
160 (B) TYPE: nucleic acid
161 (C) STRANDEDNESS: single
162 (D) TOPOLOGY: linear

W--> 164 (ii) MOLECULE TYPE: DNA
168 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

170 GGGTTTGGAA TTCCTAATAA TGTCTGTACA AGTAGAAACC 40

172 (2) INFORMATION FOR SEQ ID NO: 4:

174 (i) SEQUENCE CHARACTERISTICS:
175 (A) LENGTH: 34 base pairs
176 (B) TYPE: nucleic acid
177 (C) STRANDEDNESS: single
178 (D) TOPOLOGY: linear

W--> 180 (ii) MOLECULE TYPE: DNA
184 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

186 GGGTTTCGGG ATCCCGTCAT TCCAGTTTA GAAC 34

188 (2) INFORMATION FOR SEQ ID NO: 5:

190 (i) SEQUENCE CHARACTERISTICS:
191 (A) LENGTH: 348 base pairs
192 (B) TYPE: nucleic acid
193 (C) STRANDEDNESS: single
194 (D) TOPOLOGY: linear

196 (ii) MOLECULE TYPE: cDNA

199 (ix) FEATURE:

200 (A) NAME/KEY: CDS
201 (B) LOCATION: 14..325

204 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

206 GGAATTCTTA ATA ATG TCC GTA CAA GTA GAA ACC ATC TCC CCA GGA GAC 49

207 Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp

208 1 5 10

210 GGG CGC ACC TTC CCC AAG CGC GGC CAG ACC TGC GTG GTG CAC TAC ACC 97

211 Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr

212 15 20 25

214 GGG ATG CTT GAA GAT GGA AAG AAA TTT GAT TCC TCC CGT GAC CGT AAC

145

RAW SEQUENCE LISTING
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Input Set : N:\CrF3\RULE60\09517491.raw
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215	Gly	Met	Leu	Glu	Asp	Gly	Lys	Phe	Asp	Ser	Ser	Arg	Asp	Arg	Asn		
216	30					35				40							
218	AAG	CCC	TTT	AAG	TTT	ATG	CTA	GGC	AAG	CAG	GAG	GTG	ATC	CGA	GGC	TGG	193
219	Lys	Pro	Phe	Lys	Phe	Met	Leu	Gly	Lys	Gln	Glu	Val	Ile	Arg	Gly	Trp	
220	45					50				55			60				
222	GAA	GAA	GGG	GTT	GCC	CAG	ATG	AGT	GTG	GGT	CAG	CGT	GCC	AAA	CTG	ACT	241
223	Glu	Glu	Gly	Val	Ala	Gln	Met	Ser	Val	Gly	Gln	Arg	Ala	Lys	Leu	Thr	
224						65				70			75				
226	ATA	TCT	CCA	GAT	TAT	GCC	TAT	GGT	GCC	ACT	GGG	CAC	CCA	GGC	ATC	ATC	289
227	Ile	Ser	Pro	Asp	Tyr	Ala	Tyr	Gly	Ala	Thr	Gly	His	Pro	Gly	Ile	Ile	
228						80				85			90				
230	CCA	CCA	CAT	GCC	ACT	CTC	GTC	TTC	GAT	GTG	GAG	CTT	CTAAA	ACTGG		335	
231	Pro	Pro	His	Ala	Thr	Leu	Val	Phe	Asp	Val	Glu	Leu					
232						95			100								
234	AATGACGGGA	TCC														348	
237	(2)	INFORMATION FOR SEQ ID NO: 6:															
239	(i)	SEQUENCE CHARACTERISTICS:															
240	(A)	LENGTH: 104 amino acids															
241	(B)	TYPE: amino acid															
242	(D)	TOPOLOGY: linear															
244	(ii)	MOLECULE TYPE: protein															
246	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 6:															
248	Met	Ser	Val	Gln	Val	Glu	Thr	Ile	Ser	Pro	Gly	Asp	Gly	Arg	Thr	Phe	
249	1				5					10				15			
251	Pro	Lys	Arg	Gly	Gln	Thr	Cys	Val	Val	His	Tyr	Thr	Gly	Met	Leu	Glu	
252						20			25				30				
254	Asp	Gly	Lys	Phe	Asp	Ser	Ser	Arg	Asp	Arg	Asn	Lys	Pro	Phe	Lys		
255						35			40			45					
257	Phe	Met	Leu	Gly	Lys	Gln	Glu	Val	Ile	Arg	Gly	Trp	Glu	Glu	Gly	Val	
258						50			55			60					
260	Ala	Gln	Met	Ser	Val	Gly	Gln	Arg	Ala	Lys	Leu	Thr	Ile	Ser	Pro	Asp	
261						65			70			75			80		
263	Tyr	Ala	Tyr	Gly	Ala	Thr	Gly	His	Pro	Gly	Ile	Ile	Pro	Pro	His	Ala	
264						85			90			95					
266	Thr	Leu	Val	Phe	Asp	Val	Glu	Leu									
267				100													
270	(2)	INFORMATION FOR SEQ ID NO: 7:															
272	(i)	SEQUENCE CHARACTERISTICS:															
273	(A)	LENGTH: 48 base pairs															
274	(B)	TYPE: nucleic acid															
275	(C)	STRANDEDNESS: single															
276	(D)	TOPOLOGY: linear															
W--> 278	(ii)	MOLECULE TYPE: DNA															
282	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 7:															
284	TCGCCGGAAT	TCGGGGCGGG	AGGTGGAGGA	GTACAAGTAG	AAACCATC											48	
286	(2)	INFORMATION FOR SEQ ID NO: 8:															
288	(i)	SEQUENCE CHARACTERISTICS:															
289	(A)	LENGTH: 34 base pairs															
290	(B)	TYPE: nucleic acid															

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291	(C) STRANDEDNESS: single	
292	(D) TOPOLOGY: linear	
W--> 294	(ii) MOLECULE TYPE: DNA	
298	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
300	GGGTTTCGGG ATCCCGTCAT TCCAGTTTA GAAG	34
302	(2) INFORMATION FOR SEQ ID NO: 9:	
304	(i) SEQUENCE CHARACTERISTICS:	
305	(A) LENGTH: 41 base pairs	
306	(B) TYPE: nucleic acid	
307	(C) STRANDEDNESS: single	
308	(D) TOPOLOGY: linear	
W--> 310	(ii) MOLECULE TYPE: DNA	
314	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
316	CGCGGATCCG CGCATTATTA CTTGTTTGA TTGATTTTT G	41
318	(2) INFORMATION FOR SEQ ID NO: 10:	
320	(i) SEQUENCE CHARACTERISTICS:	
321	(A) LENGTH: 40 base pairs	
322	(B) TYPE: nucleic acid	
323	(C) STRANDEDNESS: single	
324	(D) TOPOLOGY: linear	
W--> 326	(ii) MOLECULE TYPE: DNA	
330	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
332	CGCGGATCCG CGTAAAAGCA AAGTACTATC AATTGAGCCG	40
335	(2) INFORMATION FOR SEQ ID NO: 11:	
337	(i) SEQUENCE CHARACTERISTICS:	
338	(A) LENGTH: 5430 base pairs	
339	(B) TYPE: nucleic acid	
340	(C) STRANDEDNESS: both	
341	(D) TOPOLOGY: linear	
343	(ii) MOLECULE TYPE: cDNA	
346	(ix) FEATURE:	
347	(A) NAME/KEY: CDS	
348	(B) LOCATION: 1..5427	
351	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:	
353	TG GAG CAC AGT GGG ATT GGA AGA ATC AAA GAG CAG AGT GCC CGC ATG	48
354	Leu Glu His Ser Gly Ile Gly Arg Ile Lys Glu Gln Ser Ala Arg Met	
355	1 5 10 15	
357	CTG GGG CAC CTG GTC TCC AAT GCC CCC CGA CTC ATC CGC CCC TAC ATG	96
358	Leu Gly His Leu Val Ser Asn Ala Pro Arg Leu Ile Arg Pro Tyr Met	
359	20 25 30	
361	GAG CCT ATT CTG AAG GCA TTA ATT TTG AAA CTG AAA GAT CCA GAC CCT	144
362	Glu Pro Ile Leu Lys Ala Leu Ile Leu Lys Leu Lys Asp Pro Asp Pro	
363	35 40 45	
365	GAT CCA AAC CCA GGT GTG ATC AAT GTC CTG GCA ACA ATA GGA GAA	192
366	Asp Pro Asn Pro Gly Val Ile Asn Asn Val Leu Ala Thr Ile Gly Glu	
367	50 55 60	
369	TTG GCA CAG GTT AGT GGC CTG GAA ATG AGG AAA TGG GTT GAT GAA CTT	240
370	Leu Ala Gln Val Ser Gly Leu Glu Met Arg Lys Trp Val Asp Glu Leu	
371	65 70 75 80	

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/517,491

DATE: 02/28/2002
TIME: 14:57:36

Input Set : N:\Crf3\RULE60\09517491.raw
Output Set: N:\CRF3\02282002\I517491.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:164 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:180 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4
L:278 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:294 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:310 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:326 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10
L:1705 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21
L:1721 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22
L:1775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1835 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:1858 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:1875 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:1892 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28
L:1909 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:1926 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:1943 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31
L:1960 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32
L:1977 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33
L:1994 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34
L:2021 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35